

11420122.APP
SEQUENCE LISTING

<110> Pausch, Mark H
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011

<141> 1997-03-11

<150> 07/332,312

<151> 1994-10-31

<150> PCT/US95/14364

<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

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Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
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Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
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 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
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 100 105 110
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 115 120 125
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135

140

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Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
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Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
 195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
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Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
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Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
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Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
 260 265 270

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
 275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
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115

120

125

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Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
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Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr
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Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
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Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
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460

450

455

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Trp

<210> 38
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 35 40 45
 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
 50 55 60
 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly
 65 70 75 80
 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
 85 90 95
 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
 100 105 110
 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
 115 120 125
 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
 130 135 140
 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
 145 150 155 160
 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
 165 170 175
 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
 180 185 190
 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
 195 200 205
 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
 210 215 220
 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln

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225 230 235 240
 Asp Ala Arg Ser Ala Leu Ala val val Gly Gly Lys val val Leu Val
 245 250 255
 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
 260 265 270
 Arg Glu Ala Phe Ile val Glu Asn Leu Tyr val Ser Lys His Ile Ile
 275 280 285
 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
 290 295 300
 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
 305 310 315 320
 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
 325 330 335

xaa

<210> 39
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DEGENERATE
 PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>
 <221> variation
 <222> (2)
 <223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39
 tnggatwygg wgaywyt

17

<210> 40
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DEGENERATE
 PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40
 rtcwccrwah ccdydggt

18

<210> 41
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 41
 cgcagggcaga gccacaaaga gtacacag

28

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<210> 42
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 42
 ggagatcagc taggcacccat atttgg 26

<210> 43
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 43
 atgctgcatg cctcatgctt cccagc 26

<210> 44
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 44
 gggtatttaa agagagggct 20

<210> 45
 <211> 426
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val
 1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys
 20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val
 35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr
 50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe
 65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val
 85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr
 100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly
 115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu
 130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe
 145 150 155 160

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Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile
 165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val
 180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu
 195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile
 210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu
 225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
 245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
 260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
 275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
 290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
 305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
 325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
 340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
 355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
 370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
 385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
 405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
 420 425

<210> 46

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (35)

<223> N AT POSITION 35 INDICATES UNDETERMINED
 NUCLEOTIDE

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<220>
 <221> unsure
 <222> (2057)
 <223> N AT POSITION 2057 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2067)
 <223> N AT POSITION 2067 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2111)
 <223> N AT POSITION 2111 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2120)
 <223> N AT POSITION 2120 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 46
 ccatacctaata acgactcact ataggggctcg agcgnccgcc cgggcagtaa aatgcctgcc 60
 cgtgcagctc ggagcgcgca gcccgtctct gaataagaag tgagtacaat ggcgtgtttg 120
 taaaaaaaaag cttcaagtcc gtctttttca aaaaacattt tgaatgctgc atgcctcatg 180
 cttcccagcg cctcgcggga gagaccgggc tatagagcag gagtggcggc acctgacttg 240
 ctggatccta aatctgcccgc tcagaactcc aaaccgaggc tctcattttc cacgaaaccc 300
 acagtgcctt cttcccgggt ggagagtgc acgaccatta atgttatgaa atggaagacg 360
 gtctccacga tattcctggt ggtgtctctc tatctgatca tcggagccac cgtgttcaaa 420
 gcattggagc agcctcatga gatttcacag aggaccacca ttgtgatcca gaagcaaaca 480
 ttcataatccc aacattcctg tgtcaattcg acggagctgg atgaactcat tcagcaaata 540
 gtggcagcaa taaatgcagg gattataacc ttaggaaaca cttccaatca aatcagtcac 600
 tgggatttgg gaagtctctt cttcttttgc ggcactgtta ttacaaccat aggatttggg 660
 aacatctcac cagcacaga aggcggcaaa atattctgta tcactctatgc cttactggga 720
 attccccctt ttggttttct cttggctgga gttggagatc agctaggcac catatttggg 780
 aaaggaattg ccaaagtggg agatacgttt attaagtggg atgttagtca gaccaagatt 840
 cgcatacatc caacaatcat attataacta ttgtgctgtg tactctttgt ggctctgccr 900
 gcgatcatat tcaaacacat agaaggctgg agtgccctgg acgccattta ttttgtgggt 960
 atcactctaa caactattgg atttgggtgac tacgtttgcag gtggatccga tattgaatat 1020
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 gtgggagagt tcagagcaca cgctgctgag tggagagcca acgtcacagc cgaattcaaa 1200
 gaaaccagga ggcgactgag tgtggagatt tatgacaagt tccagcgggc cacctccatc 1260
 aagcgggaagc tctcggcaga actggctgga aaccacaatc aggagctgac tctttgtagg 1320
 aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctc cttactgaag 1380
 actgagagta tctatctgaa tgggttggcg ccacactgtg ctggtgaaga gattgctgtg 1440
 attgagaaca tcaaatagcc ctctctttaa ataactttag gcatagccat aggtgaggac 1500
 ttctctatgc tctttatgac tgttgcctgg agcatttttt aaattgtgca tgagctcaaa 1560
 gggggaacaa aatagataca cccatcatgg tcatctatca tcaagagaat ttggaattct 1620
 gagccagcac tttctttctg atgatgcttg ttgaacggcc cactttcttt gatgagtggg 1680
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 tcttccctg cccccacccc taggctcacc tctgcagtct tttacccag ttctcccat 2040
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 gaaatagatg ncaaattagn tggacattga 2130

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<210> 47
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 47
 aaaagaatcta aaatgcttcc cagcgcc 27

<210> 48
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 48
 aaagtcgacc tatttgatgt tctcaat 27

<210> 49
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 49
 aaaaagctta aaatgcttcc cagcgcc 27

<210> 50
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 50
 aaatctagac tatttgatgt tctcaat 27

<210> 51
 <211> 534
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (262)
 <223> N AT POSITION 262 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 51
 aacaaaaacc ttttttgttt tgaatggcct agagagggta agggatcccc tgacgaacag 60
 gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120
 gcggaaggca gtattgggggt aggcaggac cccagcagac atggcactca gagctctcac 180
 tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240
 aaggccttct gcatggctct antagccctt gggctgcccag cctccttagc tctcgtggcc 300
 accctgcgcc attgcctgct gcctgtgctc agccgcccac gtgcctgggt agcgggtccac 360
 tggcagctgt caccggccag ggctgcgctg ctgcaggcag ttgcactggg actgctgggtg 420
 gccagcagct ttgtgctgct gccagcgtg gtgctgtggg gccttcaggg cgactgcagc 480
 ctgctg999g ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52
 <211> 956
 <212> DNA

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<213> Mus musculus

<400> 52

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atgatacgaat ttaatacgaac tcaactatagg gaattttggcc ctcgaggcca agaatttcggc 60
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gcgcgcgggt gttcgcagca ctggagtcgg agccggagat gatcgagcgg cagcgggtcg 180
agctgcggca gctggagctg cgggcgcgct acaacctcag cgagggcggc tacgaggagc 240
tggagcgcgt cgtgctgcgc ctcaagccgc acaaggccgg cgtgcagtgg cgcttcgccg 300
gttccttcta cttcgccatc accgtcatca ccaccatcgg ctatggtcac gcggcgccca 360
gcacggacgg aggcaagggtg ttctgcatgt tctacgcgct gctgggcacg ccgctcacac 420
tagtcatgtt ccagagcctg ggtgaacgca tcaacacctc cgtgaggtac ctgctgcacc 480
gtgccaaagag ggggctgggc atgcggcacg ccgaagtgtc catggccaac atggtgctca 540
tcggtttcgt gtcgtgcacg agcacgctgt gcacgcggcg agctgccttc tcctactacg 600
agcgcctggac tttcttccag gcctattact actgcttcac caccctcacc accatcggct 660
tcggcgacta tgtggcgctg cagaaggacc aggcgctgca gacgcagccg cagtatgtgg 720
cttcagcttc gtgtacatcc tcacgggctc acggtcatcg gcgcttcctc aacctcgtgg 780
cttcgcgatt catgacatg aacgcccagg acgagaagcg tgatgcggag caccgcgccc 840
tgctcacgca caacggccag gctgtcggcc tgggtggcct gagctgcctg agcggtagcc 900
tgggcgacgg cgtgcgtccc cgcgaccag tcacatgcgc tcgggccgca agctta 956

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<210> 53

<211> 1055

<212> DNA

<213> Mus musculus

<220>

<221> unsure

<222> (247)

<223> N AT POSITION 247 INDICATES UNDETERMINED NUCLEOTIDE

<220>

<221> unsure

<222> (593)

<223> N AT POSITION 593 INDICATES UNDETERMINED NUCLEOTIDE

<220>

<221> unsure

<222> (952)

<223> N AT POSITION 952 INDICATES UNDETERMINED NUCLEOTIDE

<400> 53

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ctgaaaccat gggcccgata cctgctcctg cttatggccc acctgctggc catgggcctt 60
ggggctgtgg tgcttcaggc cctggagggc cctccagctc gccacctcca ggcccaggct 120
caggctgaac tggctagctt ccaggcagag cacaggccct gcttgccacc tgaggccctg 180
gaggagctgc taggtgcggt cctgagagca caggcccatg gagtttccag cctgggcaac 240
agctcanaga caagcaactg ggatctgccc tcagctctgc tgttcaactg cagcatcctc 300
accaccaccg gttatggcca catggcccca ctctcctcag gtggaaggc cttctgtgtg 360
gtctatgcag cccttgggct gccagcctct ctagcacttg tggctgccct gcgccactgc 420
ttgctgcctg tgttcagtcg cccagggtgac tgggtagcca ttcgctggca gctggcacca 480
gtcaggctg ctctgtaca ggcagcagga ctgggcctcc tgggtggcctg tgccttcagt 540
ctgctgccag cactggtgct gtggggtgta cagggtgact ggcagcctgc tanaaccatc 600
tacttctgtt tcggctcact cagcacgacg ggcctaggag acttgctgcc tgcccatgga 660
cgtggcctgc acccagccat ttaccacctt gggcagtttg cacttcttgg ttacttgctc 720
ctggggctcc tggccatggt gttagcagta gagaccttct cagagctgcc tcaggctccgt 780
gccatggtga aattctttgg gccagtgggc tctagaaccg atgaagatca agatggcatc 840
ctaggccaag atgagctggc tctgagcact gtgctgcctg acgccccagt cttgggacca 900
accacccag cctgagcggg aggcaccaag gaggcttga agaacaatagc angaagggtt 960
atgggaatga atatgtcatg ggataatgtt aattttaaaa attaaatggg ctgcttagca 1020
tgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1055

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<210> 54
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (88)
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
 1 5 10 15
 Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
 20 25 30
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
 35 40 45
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
 50 55 60
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
 65 70 75 80
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
 85 90 95
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
 100 105 110
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
 115 120 125
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
 130 135 140
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
 145 150 155 160
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
 165 170 175
 Leu Gly

<210> 55
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 55
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
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35

40

45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
 85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
 290 295 300

Ala Ala Ala Ser Leu
 305

<210> 56
 <211> 304
 <212> PRT
 <213> MUS musculus

<220>
 <221> UNSURE
 <222> (83)
 <223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE
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<220>

<221> UNSURE

<222> (198)

<223> N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

<400> 56

Leu Lys Pro Trp Ala Arg Tyr Leu Leu Leu Leu Met Ala His Leu Leu
 1 5 10 15

Ala Met Gly Leu Gly Ala Val Val Leu Gln Ala Leu Glu Gly Pro Pro
 20 25 30

Ala Arg His Leu Gln Ala Gln Val Gln Ala Glu Leu Ala Ser Phe Gln
 35 40 45

Ala Glu His Arg Ala Cys Leu Pro Pro Glu Ala Leu Glu Glu Leu Leu
 50 55 60

Gly Ala Val Leu Arg Ala Gln Ala His Gly Val Ser Ser Leu Gly Asn
 65 70 75 80

Ser Ser Xaa Thr Ser Asn Trp Asp Leu Pro Ser Ala Leu Leu Phe Thr
 85 90 95

Ala Ser Ile Leu Thr Thr Thr Gly Tyr Gly His Met Ala Pro Leu Ser
 100 105 110

Ser Gly Gly Lys Ala Phe Cys Val Val Tyr Ala Ala Leu Gly Leu Pro
 115 120 125

Ala Ser Leu Ala Leu Val Ala Ala Leu Arg His Cys Leu Leu Pro Val
 130 135 140

Phe Ser Arg Pro Gly Asp Trp Val Ala Ile Arg Trp Gln Leu Ala Pro
 145 150 155 160

Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala
 165 170 175

Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly
 180 185 190

Asp Trp Gln Pro Ala Xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser
 195 200 205

Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His
 210 215 220

Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu
 225 230 235 240

Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu
 245 250 255

Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg
 260 265 270

Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu
 275 280 285

Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala
 290 295 300

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<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)..(9)
<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT
POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8
IS Y, F, V, I, M, OR L

<220>
<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<400> 57
Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>
<221> VARIANT
<222> (1)..(8)
<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I,
V, L, F, OR Y

<400> 58
Xaa Xaa Xaa Gly Xaa Pro xaa
1 5

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<400> 59
Tyr Ala Leu Leu Gly Ile Pro
1 5

<210> 60
<211> 7

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (6)

<223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60

Tyr Ala Leu Leu Gly Xaa Pro
1 5

<210> 61

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Gly

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<210> 62
 <211> 309
 <212> PRT
 <213> Mus-musculus

<400> 62
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
 35 40 45
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
 85 90 95
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
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300

290

295

Ala Ala Ala Ser Leu
305

<210> 63

<211> 434

<212> PRT

<213> Caenorhabditis elegans

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala
1 5 10 15Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val
20 25 30Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro
35 40 45Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp
50 55 60Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro
65 70 75 80Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro
85 90 95Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu
100 105 110Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser
115 120 125Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn
130 135 140Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp
145 150 155 160Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys
165 170 175Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn
180 185 190Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val
195 200 205Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp
210 215 220Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala
225 230 235 240Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
245 250 255Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
260 265 270

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Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
 275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
 290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val
 305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
 325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg
 340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
 355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
 370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
 385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
 405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
 420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
 CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
 S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,
 L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro
 1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence between Ce orf1 and Dm orf1

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<400> 65
Thr Trp Thr Phe
1

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

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Gly Tyr Gly Asn
1

32
<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 67
Gly Phe Gly Asp
1
